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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=10; day=29; hr=11; min=4; sec=37; ms=285;]

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Application No: 10562021 Version No: 3.0

Input Set:

Output Set:

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Finished: 2008-09-30 15:57:27.347
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 112 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

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W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

SEQUENCE LISTING

<110> Svendsen, Allan
Beier, Lars
Spendler, Tina
Jensen, Morten Tovborg
Jorgensen, Christel Thea

<120> CGTASE VARIANTS

<130> 10340-204-US

<140> 10562021
<141> 2006-01-11

<150> DK PCT/DK2004/000468
<151> 2004-07-01

<150> DK PA 2003 00994
<151> 2003-07-01

<150> US 60/484,004
<151> 2003-07-01

<160> 20

<170> PatentIn version 3.5

<210> 1
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<213> Bacillus agaradherens

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Asn Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
35 40 45

Asp Gly Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
50 55 60

Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Gly Cys Lys Asn Leu
65 70 75 80

Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
85 90 95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
100 105 110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Ser Gly Thr Thr
115 120 125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
130 135 140

Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145 150 155 160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
165 170 175

Ala Asp Phe Asp Asn Pro Asn Tyr Ala Glu Asn Gly Ile Leu Tyr Asp
180 185 190

Asn Gly Asn Tyr Val Ser Ser Tyr Ser Asp Asn Ser Asp Leu Phe Leu
195 200 205

Tyr Asn Gly Gly Thr Asp Phe Ser Thr Tyr Glu Asp Glu Ile Tyr Arg
210 215 220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ala Glu Leu Asn
225 230 235 240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
245 250 255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Gln Lys
260 265 270

Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly
275 280 285

Glu Trp Phe Thr Gly Pro Tyr Gly Asn Glu Asp Tyr Thr Lys Phe Ala
290 295 300

Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr
305 310 315 320

Arg Asn Val Ile Gly Asn Asn Asn Gly Thr Met Tyr Asp Ile Glu Lys
325 330 335

Met Leu Thr Asp Thr Glu Asn Asp Tyr Asp Arg Pro Gln Asp Gln Val
340 345 350

Thr Phe Leu Asp Asn His Asp Met Ser Arg Phe Thr Asn Asp Gly Glu
355 360 365

Ser Thr Arg Thr Thr Asp Ile Gly Leu Ala Leu Met Leu Thr Ser Arg
370 375 380

Gly Val Pro Thr Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Glu Gly Asp
385 390 395 400

Gly Asp Pro Gly Ser Arg Gly Met Met Glu Ser Phe Gly Glu Asn Thr
405 410 415

Asp Ala Tyr Lys Leu Ile Gln Lys Leu Ala Pro Leu Arg Lys Ser Asn
420 425 430

Pro Ala Tyr Gly Tyr Gly Thr Thr Lys Glu Arg Trp Ile Asn Asp Asp
435 440 445

Val Ile Ile Tyr Glu Arg Asn Phe Gly Asp Asn Tyr Ala Leu Ile Ala
450 455 460

Ile Asn Arg Asn Leu Asn Thr Ser Tyr Asn Ile Gln Gly Leu Gln Thr
465 470 475 480

Glu Met Pro Ser Asn Ser Tyr Asp Asp Val Leu Asp Gly Leu Leu Asp
485 490 495

Gly Gln Ser Ile Val Val Asp Asn Asn Gly Glu Val Asn Glu Phe Gln
500 505 510

Met Ser Pro Gly Glu Val Gly Val Trp Glu Phe Glu Ala Thr Asn Val
515 520 525

Asp Lys Pro Ser Ile Gly Gln Val Gly Pro Ile Ile Gly Glu Ala Gly
530 535 540

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Pro Gly Thr
545 550 555 560

Val Gln Phe Gly Ser Thr Ser Ala Glu Ile Val Ser Trp Asn Asp Thr
565 570 575

Val Ile Ile Ile Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
580 585 590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
595 600 605

Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
610 615 620

Glu Thr Lys Met Gly Glu Asn Ile Phe Leu Val Gly Asn Val His Glu
625 630 635 640

Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
645 650 655

Val Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
660 665 670

Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
675 680 685

Val Thr Trp Gln Ser Gly Ala Asn His Thr Tyr Ser Ser Pro Glu Ser
690 695 700

Gly Thr Gly Ile Ile Arg Val Asp Trp
705 710

<210> 2

<211> 713

<212> PRT

<213> Bacillus agaradherens

<400> 2

Met Arg Lys Lys Thr Leu Lys Arg Leu Leu Thr Leu Val Val Gly Leu
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Ser Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
35 40 45

Asp Val Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
50 55 60

Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Asp Cys Lys Asn Leu
65 70 75 80

Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
85 90 95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
100 105 110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Phe Gly Thr Thr
115 120 125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
130 135 140

Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145 150 155 160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
165 170 175

Ala Asp Phe Asp Asn Pro Asp Tyr Ala Glu Asn Gly Val Leu Tyr Asp
180 185 190

Asp Gly Asn Tyr Leu Gly Ser Tyr Ser Asp Asp Ser Asp Leu Phe Leu
195 200 205

Tyr Asn Gly Gly Thr Asp Phe Ser Asn Tyr Glu Asp Glu Ile Tyr Arg
210 215 220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ser Glu Leu Asn
225 230 235 240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
245 250 255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Lys Lys
260 265 270

Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly
275 280 285

Glu Trp Phe Thr Gly Pro Ser Gly Asn Glu Asp Tyr Thr Lys Phe Ala
290 295 300

Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr
305 310 315 320

Arg Asn Val Ile Gly Asn Asn Asn Gly Thr Met Tyr Asp Ile Glu Lys
325 330 335

Met Leu Thr Asp Thr Glu Asn Asp Tyr Asp Arg Pro Gln Asp Gln Val
340 345 350

Thr Phe Leu Asp Asn His Asp Met Ser Arg Phe Thr Asn Gly Gly Glu
355 360 365

Ser Thr Arg Thr Thr Asp Ile Gly Leu Ala Leu Met Leu Thr Ser Arg
370 375 380

Gly Val Pro Thr Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Lys Gly Asp
385 390 395 400

Gly Asp Pro Gly Ser Arg Gly Met Met Ala Ser Phe Asp Glu Asn Thr
405 410 415

Asp Ala Tyr Lys Leu Ile Gln Lys Leu Ala Pro Leu Arg Lys Ser Asn
420 425 430

Pro Ala Tyr Gly Tyr Gly Thr Thr Glu Arg Trp Ile Asn Asp Asp
435 440 445

Val Leu Ile Tyr Glu Arg His Phe Gly Glu Asn Tyr Ala Leu Ile Ala
450 455 460

Ile Asn Arg Ser Leu Asn Thr Ser Tyr Asn Ile Gln Gly Leu Gln Thr
465 470 475 480

Glu Met Pro Ser Asn Ser Tyr Asp Asp Val Leu Asp Gly Leu Leu Asp
485 490 495

Gly Gln Ser Ile Val Val Asp Asn Lys Gly Gly Val Asn Glu Phe Gln
500 505 510

Met Ser Pro Gly Glu Val Ser Val Trp Glu Phe Glu Ala Glu Asn Val
515 520 525

Asp Lys Pro Ser Ile Gly Gln Val Gly Pro Ile Ile Gly Glu Ala Gly
530 535 540

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Gln Gly Thr
545 550 555 560

Val His Phe Gly Ser Thr Ser Ala Glu Ile Leu Ser Trp Asn Asp Thr
565 570 575

Ile Ile Thr Leu Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
580 585 590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
595 600 605

Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
610 615 620

Glu Thr Lys Leu Gly Glu Asn Val Phe Leu Val Gly Asn Val His Glu
625 630 635 640

Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
645 650 655

Ile Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
660 665 670

Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
675 680 685

Val Ile Trp Gln Ser Gly Ala Asn Gln Thr Tyr Ser Ser Pro Glu Ser
690 695 700

Gly Thr Gly Ile Ile Arg Val Asp Trp

705

710

<210> 3

<211> 714

<212> PRT

<213> Panibacillus macerans

<400> 3

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20 25 30

Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
35 40 45

Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
50 55 60

Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65 70 75 80

Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
85 90 95

Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
100 105 110

Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
115 120 125

Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
130 135 140

Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145 150 155 160

Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
165 170 175

Gly Phe Ala Glu Asn Gly Gly Met Tyr Asp Asn Gly Ser Leu Leu Gly
180 185 190

Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
195 200 205

Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
210 215 220

Ala Asp Ile Asn His Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225 230 235 240

Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
245 250 255

Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
260 265 270

Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
275 280 285

Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
290 295 300

Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305 310 315 320

Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
325 330 335

Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
340 345 350

Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
355 360 365

Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
370 375 380

Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385 390 395 400

Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
405 410 415

Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
420 425 430

Ala Tyr Gly Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
435 440 445

Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
450 455 460

Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro
465 470 475 480

Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
485 490 495

Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
500 505 510

Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
515 520 525

Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
530 535 540

Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545 550 555 560

Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
565 570 575

Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
580 585 590

Val Lys Thr Se